

Deep learning in cancer pathology: a new generation of clinical biomarkers

Year: 2020 | Citations: 518 | Authors: A. Echle, Niklas Rindtorff, T. Brinker, Tom Luedde, A. Pearson

Abstract

Clinical workflows in oncology rely on predictive and prognostic molecular biomarkers. However, the growing number of these complex biomarkers tends to increase the cost and time for decision-making in routine daily oncology practice; furthermore, biomarkers often require tumour tissue on top of routine diagnostic material. Nevertheless, routinely available tumour tissue contains an abundance of clinically relevant information that is currently not fully exploited. Advances in deep learning (DL), an artificial intelligence (AI) technology, have enabled the extraction of previously hidden information directly from routine histology images of cancer, providing potentially clinically useful information. Here, we outline emerging concepts of how DL can extract biomarkers directly from histology images and summarise studies of basic and advanced image analysis for cancer histology. Basic image analysis tasks include detection, grading and subtyping of tumour tissue in histology images; they are aimed at automating pathology workflows and consequently do not immediately translate into clinical decisions. Exceeding such basic approaches, DL has also been used for advanced image analysis tasks, which have the potential of directly affecting clinical decision-making processes. These advanced approaches include inference of molecular features, prediction of survival and end-to-end prediction of therapy response. Predictions made by such DL systems could simplify and enrich clinical decision-making, but require rigorous external validation in clinical settings.